

RESEARCH ARTICLE

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Complete chloroplast genome of *Gracilaria firma* (Gracilariaceae, Rhodophyta), with discussion on the use of chloroplast phylogenomics in the subclass Rhodymeniophycidae

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Abstract

Background: The chloroplast genome of *Gracilaria firma* was sequenced in view of its role as an economically important marine crop with wide industrial applications. To date, there are only 15 chloroplast genomes published for the Florideophyceae. Apart from presenting the complete chloroplast genome of *G. firma*, this study also assessed the utility of genome-scale data to address the phylogenetic relationships within the subclass Rhodymeniophycidae. The synteny and genome structure of the chloroplast genomes across the taxa of Eurhodophytina was also examined.

Results: The chloroplast genome of *Gracilaria firma* maps as a circular molecule of 187,001 bp and contains 252 genes, which are distributed on both strands and consist of 35 RNA genes (3 rRNAs, 30 tRNAs, tmRNA and a ribonuclease P RNA component) and 217 protein-coding genes, including the unidentified open reading frames. The chloroplast genome of *G. firma* is by far the largest reported for Gracilariaceae, featuring a unique intergenic region of about 7000 bp with discontinuous vestiges of red algal plasmid DNA sequences interspersed between the *nbIA* and *cpeB* genes. This chloroplast genome shows similar gene content and order to other Florideophycean taxa. Phylogenomic analyses based on the concatenated amino acid sequences of 146 protein-coding genes confirmed the monophyly of the classes Bangiophyceae and Florideophyceae with full nodal support. Relationships within the subclass Rhodymeniophycidae in Florideophyceae received moderate to strong nodal support, and the monotypic family of Gracilariales were resolved with maximum support.

Conclusions: Chloroplast genomes hold substantial information that can be tapped for resolving the phylogenetic relationships of difficult regions in the Rhodymeniophycidae, which are perceived to have experienced rapid radiation and thus received low nodal support, as exemplified in this study. The present study shows that chloroplast genome of *G. firma* could serve as a key link to the full resolution of *Gracilaria sensu lato* complex and recognition of *Hydropuntia* as a genus distinct from *Gracilaria sensu stricto*.

Keywords: Chloroplast genome, *Gracilaria firma*, Gracilariaceae, Conserved synteny, Phylogenomic analyses, Red algal plasmid remnants

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